

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Seed, Brian et al.

(ii) TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES AND METHODS

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

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- (C) CITY: Boston
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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/756,018
- (B) FILING DATE: 25-NOV-96
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/661,960
- (B) FILING DATE: 12-JUN-1996

(viii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/000,213
- (B) FILING DATE: 14-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

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- (C) REFERENCE/DOCKET NUMBER: 00786/284002

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Thr Asn Ser Leu Glu Thr Ser Thr Gly Thr Ser Gly Pro Pro
1 5 10 15

Val Thr

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu Gly Pro
1 5 10 15

Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp
20 25 30

Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro
35 40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe
1 5 10 15
Leu Pro Glu Thr
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Asp Arg Arg Gln Ala Thr Glu Phe Glu Phe Leu Asp Phe Asp Phe
1 5 10 15
Leu Pro Glu Thr
20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Asp Arg Arg Gln Ala Ala Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe
1 5 10 15
Leu Pro Glu Ala
20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

1	5	10	15
Arg	Asp	Arg	Arg
Gln	Ala	Ala	Glu
Phe	Glu	Phe	Leu
Asp	Phe	Asp	Phe
			Phe
Leu	Pro	Glu	Ala
			20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 2287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCTTACCA CCATGGACTG GACCTGGAGG TTCCCTTTCT TTGTGGTGGC AGCAGCTACA	60
GGTGTCCAGT CCCAGGTGCA GCTGGTGCAG TCTGGGCTG AGGTGAAGAA GCCTGGGTCC	120
TCGGTGAAAGG TCTCCTGCAA GGCTTCTGGA GGCACCTTCA GCAGCTATGC TATCAGCTGG	180
GTGCGACAGG CCCCTGGACA AGGGCTTGAG TGGATGGGAG GGATCATCCC TATCTTTGGT	240
ACAGCAAACACT ACGCACAGAA GTTCCAGGGC AGAGTCACGA TTACCGCGGA CGAATCCACG	300
AGCACACGCCT ACATGGAGCT GAGCAGCCTG AGATCTGAGG ACACGGCCGT GTATTACTGT	360
GCGAGAGATA ATGGAGCGTA TTGTAGTGGT GGTAGCTGCT ACTCGGGCTG GTTCGACCCC	420
TGGGGCCAGG GAACCCTGGT CACCGTCTCT TCAGGTGAGT ACTGAATTCT AGCTTCTGG	480
GGCAGGCCAG GCCTGACCTT GGCTTTGGGG CAGGGAGGGG GCTAAGGTGA GGCAGGTGGC	540
GCCAGCAGGT GCACACCCAA TGCCCATGAG CCCAGACACT GGACGCTGAA CCTCGCGGAC	600
AGTTAAGAAC CCAGGGCCT CTGCGCCTGG GCCCAGCTCT GTCCCACACC GCGGTACAT	660
GGCACCCACCT CTCTTGCAGC CTCCACCAAG GGCCCATCGG TCTTCCCCCT GGCACCCCTCC	720
TCCAAGAGCA CCTCTGGGGG CACAGCGGCC CTGGGCTGCC TGGTCAAGGA CTACTTCCCC	780

GAACCGGTGA CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG	840
GCTGTCCTAC AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACCGT GCCCTCCAGC	900
AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTG	960
GACAAGAAAG TTGGTGAGAG GCCAGCACAG GGAGGGAGGG TGTCTGCTGG AAGCAGGCTC	1020
AGCGCTCCTG CCTGGACGCA TCCCAGCTAT GCAGCCCCAG TCCAGGGCAG CAAGGCAGGC	1080
CCCGTCTGCC TCTTCACCCG GAGCCTCTGC CCGCCCCACT CATGCTCAGG GAGAGGGTCT	1140
TCTGGCTTT TCCCAGGCTC TGGGCAGGCA CAGGCTAGGT GCCCCTAACCC CAGGCCCTGC	1200
ACACAAAGGG GCAGGTGCTG GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCCTGC	1260
CCCTGACCTA AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT	1320
CTCCTCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCAAAT CTTGTGACAA	1380
AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG GCCTCGCCCT CCAGCTCAAG	1440
GCGGGACAGG TGCCCTAGAG TAGCCTGCAT CCAGGGACAG GCCCCAGCCG GGTGCTGACA	1500
CGTCCACCTC CATCTCTTCC TCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT	1560
TCCCCCCTAA ACCCAAGGAC ACCCTCATGA TCTCCGGAC CCCTGAGGTC ACATGCGTGG	1620
TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG GACGGCGTGG	1680
AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG TACCGGGTGG	1740
TCAGCGTCCT CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC AAGTGCAGG	1800
TCTCCAACAA AGCCCTCCCA GCCCCATCG AGAAAACCCT CTCCAAAGCC AAAGGTGGGA	1860
CCCGTGGGGT GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCCCTC TGCCCTGAGA	1920
GTGACCGCTG TACCAACCTC TGTCTACAG GGCAGCCCCG AGAACACAG GTGTACACCC	1980
TGCCCTCATC CCGGGATGAG CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG	2040
GCTTCTATCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAACT	2100
ACAAGACCAC GCCTCCCGTG CTGGACTCCG ACGGCTCCTT CTTCTCTAC AGCAAGCTCA	2160
CCGTGGACAA GAGCAGGTGG CAGCAGGGGA ACGTCTCTC ATGCTCCGTG ATGCATGAGG	2220
CTCTGCACAA CCACTACACG CAGAAGAGCC TCTCCCTGTC TCCGGTAAA TGAGTGCAG	2280
GGCCGGC	2287

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Leu Thr Thr Met Asp Trp Thr Trp Arg Phe Leu Phe Phe Val Val
1 5 10 15

Ala Ala Ala Thr Gly Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly
20 25 30

Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
35 40 45

Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala
50 55 60

Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly
65 70 75 80

Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala
85 90 95

Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser
100 105 110

Cys Tyr Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
115 120 125

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
130 135 140

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
145 150 155 160

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
165 170 175

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
180 185 190

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Asp Lys
195 200 205

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
210 215 220

Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
225															240
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
			245									250			255
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
			260									265			270
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
			275									280			285
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
	290											295			300
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
	305										315				320
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
												325			335
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
												345			350
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
											355			365	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
											370			380	
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
											385			395	400
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
											405			410	415
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
											420			425	430
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
											435			440	

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1894 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGGCGCTGT CCTGGGTTCT TACAGTCCTG AGCCTCCTAC CTCTGCTGGA AGCCCAGATC	60
CCATTGTGTG CCAACCTAGT ACCGGTGCCC ATCACCAACG CCACCCCTGGA CCAGATCACT	120
GGCAAGTGGT TTTATATCGC ATCGGCCTT CGAAACGAGG AGTACAATAA GTCGGTTCAG	180
GAGATCCAAG CAACCTTCTT TTACTTCACC CCCAACAAAGA CAGAGGACAC GATCTTCAG	240
AGAGAGTACC AGACCCGACA GGACCAGTGC ATCTATAACA CCACCTACCT GAATGTCCAG	300
CGGGAAAATG GGACCATCTC CAGATACGTG GGAGGCCAAG AGCATTGCGC TCACTTGCTG	360
ATCCTCAGGG ACACCAAGAC CTACATGCTT GCTTTGACG TGAACGATGA GAAGAACTGG	420
GGGCTGTCTG TCTATGCTGA CAAGCCAGAG ACGACCAAGG AGCAACTGGG AGAGTTCTAC	480
GAAGCTCTCG ACTGCTTGCG CATTCCAAG TCAGATGTCG TGTACACCGA TTGGAAAAAG	540
GATAAGTGTG AGCCACTGGA GAAGCAGCAC GAGAAGGAGA GGAAACAGGA GGAGGGGGAA	600
TCGGATCCCC AGGGTGAGTA CTAAGCTTCA GCGCTCCTGC CTGGACGCAT CCCGGCTATG	660
CAGCCCCAGT CCAGGGCAGC AAGGCAGGCC CCGTCTGCCT CTTCACCCGG AGCCTCTGCC	720
CGCCCCACTC ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCAGGCTCT GGGCAGGCAC	780
AGGCTAGGTG CCCCTAACCC AGGCCCTGCA CACAAAGGGG CAGGTGCTGG GCTCAGACCT	840
GCCAAGAGCC ATATCCGGGA GGACCCTGCC CCTGACCTAA GCCCACCCCA AAGGCCAAC	900
TCTCCACTCC CTCAGCTCGG ACACCTTCTC TCCTCCCAGA TTCCAGTAAC TCCCAATCTT	960
CTCTCTGCAG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCACCGTG CCCAGGTAAG	1020
CCAGCCCCAGG CCTCGCCCTC CAGCTCAAGG CGGGACAGGT GCCCTAGAGT AGCCTGCATC	1080
CAGGGACAGG CCCCAGCCGG GTGCTGACAC GTCCACCTCC ATCTCTTCC CAGCACCTGA	1140
ACTCCTGGGG GGACCGTCAG TCTTCCTCTT CCCCCCAAAA CCCAAGGACA CCCTCATGAT	1200
CTCCCGGACC CCTGAGGTCA CATGCGTGGT GGTGGACGTG AGCCACGAAG ACCCTGAGGT	1260
CAAGTTCAAC TGGTACGTGG ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGGA	1320
GGAGCAGTAC AACAGCACGT ACCGGGTGGT CAGCGTCCTC ACCGTCTGC ACCAGGACTG	1380
GCTGAATGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA GCCCTCCCAG CCCCCATCGA	1440
GAAAACCATC TCCAAAGCCA AAGGTGGGAC CCGTGGGTG CGAGGGCCAC ATGGACAGAG	1500
GCCGGCTCGG CCCACCCCTCT GCCCTGAGAG TGACCGCTGT ACCAACCTCT GTCCTACAGG	1560
GCAGCCCCGA GAACCACAGG TGTACACCCCT GCCCCCCATCC CGGGATGAGC TGACCAAGAA	1620

CCAGGTCAGC CTGACCTGCC TGGTCAAAGG CTTCTATCCC AGCGACATCG CCGTGGAGTG	1680
GGAGAGCAAT GGGCAGCCGG AGAACAACTA CAAGACCACG CCTCCCGTGC TGGACTCCGA	1740
CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC AGCAGGGAA	1800
CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC CACTACACGC AGAAGAGCCT	1860
CTCCCTGTCT CCGGGTAAAT GAGTGCAGC GCCG	1894

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Leu Ser Trp Val Leu Thr Val Leu Ser Leu Leu Pro Leu Leu			
1	5	10	15

Glu Ala Gln Ile Pro Leu Cys Ala Asn Leu Val Pro Val Pro Ile Thr			
20	25	30	

Asn Ala Thr Leu Asp Gln Ile Thr Gly Lys Trp Phe Tyr Ile Ala Ser			
35	40	45	

Ala Phe Arg Asn Glu Glu Tyr Asn Lys Ser Val Gln Glu Ile Gln Ala			
50	55	60	

Thr Phe Phe Tyr Phe Thr Pro Asn Lys Thr Glu Asp Thr Ile Phe Leu
65 70 75 80

Arg Glu Tyr Gln Thr Arg Gln Asp Gln Cys Ile Tyr Asn Thr Thr Tyr
85 90 95

Leu Asn Val Gln Arg Glu Asn Gly Thr Ile Ser Arg Tyr Val Gly Gly
100 105 110

Gln Glu His Phe Ala His Leu Leu Ile Leu Arg Asp Thr Lys Thr Tyr
115 120 125

Met Leu Ala Phe Asp Val Asn Asp Glu Lys Asn Trp Gly Leu Ser Val
130 135 140

Tyr Ala Asp Lys Pro Glu Thr Thr Lys Glu Gln Leu Gly Glu Phe Tyr
145 150 155 160

Glu Ala Leu Asp Cys Leu Arg Ile Pro Lys Ser Asp Val Val Tyr Thr
165 170 175

Asp Trp Lys Lys Asp Lys Cys Glu Pro Leu Glu Lys Gln His Glu Lys
180 185 190

Glu Arg Lys Gln Glu Glu Gly Glu Ser Asp Pro Glu Gly Glu Pro Lys
195 200 205

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
210 215 220

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
225 230 235 240

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
245 250 255

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
260 265 270

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
275 280 285

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
290 295 300 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
305 310 315 320

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
325 330 335

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
340 345 350

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
355 360 365
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
370 375 380
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
385 390 395 400
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
405 410 415
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
420 425 430
Leu Ser Pro Gly Lys
435

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Leu Thr Thr Met Asp Trp Thr Trp Arg Phe Leu Phe Phe Val Val
1 5 10 15
Ala Ala Ala Thr Gly Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly
20 25 30
Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
35 40 45
Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala
50 55 60
Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly
65 70 75 80
Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala
85 90 95
Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser
100 105 110

Cys Tyr Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
115 120 125

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
130 135 140

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
145 150 155 160

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
165 170 175

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
180 185 190

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asp Lys
195 200 205

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
210 215 220

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
225 230 235 240

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
245 250 255

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Asn Phe Ser Trp
260 265 270

Tyr Val Asp Gly Val Glu Val His Asn Asn Lys Thr Lys Pro Arg Glu
275 280 285

Glu Asn Tyr Ser Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
290 295 300

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Asn Val Ser Asn
305 310 315 320

Lys Ala Leu Pro Ala Pro Ile Glu Lys Asn Ile Ser Lys Ala Lys Gly
325 330 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
340 345 350

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
355 360 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
370 375 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
385 390 395 400

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
405 410 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
420 425 430

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Glu Met Leu Arg Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly
1 5 10 15

Pro Gly Thr Pro Glu Ser Thr Thr Val Glu Pro Ala Ala Arg Arg Ser
20 25 30

Thr Gly Leu Asp Ala Gly Gly Ala Val Thr Glu
35 40

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu Ser Thr Asp Ser Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Asp Tyr Glu Tyr Asp Glu Leu Pro
1 5